#4

SEQUENCE LISTING

<110> JORGE H. CAPDEVILA, MICHAEL WATERMAN, AND VIJAKUMAR HOLLA

<120> COMPOSITIONS AND METHODS RELATING TO HYPERTENSION

<130> 22000.0110U2

<150> 60/228,947
<151> 2000-08-29

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 4123
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note = synthetic construct

<221> misc_feature
<222> (1)...(4123)
<223> n = g, a, c or t(u)

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<210> 2
<211> 507
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
synthetic construct

<400> 2

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Met Gly Phe Phe Val Phe Ser Pro Thr Arg Tyr Leu Asp Gly Ile Ser
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Gly Phe Phe Gln Trp Ala Phe Leu Leu Ser Leu Phe Leu Val Leu Phe
            20                  25                  30
Lys Ala Val Gln Phe Tyr Leu Arg Arg Gln Trp Leu Leu Lys Thr Leu
        35                  40                  45
```

```
Gln His Phe Pro Cys Met Pro Ser His Trp Leu Trp Gly His His Leu
    50                  55                  60
Lys Asp Lys Glu Leu Gln Gln Ile Leu Ile Trp Val Glu Lys Phe Pro
65                  70                  75                  80
Ser Ala Cys Leu Gln Cys Leu Ser Gly Ser Asn Ile Arg Val Leu Leu
                85                  90                  95
Tyr Asp Pro Asp Tyr Val Lys Val Val Leu Gly Arg Ser Asp Pro Lys
            100                 105                 110
Ala Ser Gly Ile Tyr Gln Phe Phe Ala Pro Trp Ile Gly Tyr Gly Leu
        115                 120                 125
Leu Leu Leu Asn Gly Lys Lys Trp Phe Gln His Arg Arg Met Leu Thr
    130                 135                 140
Pro Ala Phe His Tyr Asp Ile Leu Lys Pro Tyr Val Lys Ile Met Ala
145                 150                 155                 160
Asp Ser Val Asn Ile Met Leu Asp Lys Trp Glu Lys Leu Asp Gly Gln
                165                 170                 175
Asp His Pro Leu Glu Ile Phe His Cys Val Ser Leu Met Thr Leu Asp
            180                 185                 190
Thr Val Met Lys Cys Ala Phe Ser Tyr Gln Gly Ser Val Gln Leu Asp
        195                 200                 205
Glu Asn Ser Lys Leu Tyr Thr Lys Ala Val Glu Asp Leu Asn Asn Leu
    210                 215                 220
Thr Phe Phe Arg Leu Arg Asn Ala Phe Tyr Lys Tyr Asn Ile Ile Tyr
225                 230                 235                 240
Asn Met Ser Ser Asp Gly Arg Leu Ser His His Ala Cys Gln Ile Ala
                245                 250                 255
His Glu His Thr Asp Gly Val Ile Lys Met Arg Lys Ser Gln Leu Gln
            260                 265                 270
Asn Glu Glu Glu Leu Gln Lys Ala Arg Lys Lys Arg His Leu Asp Phe
        275                 280                 285
Leu Asp Ile Leu Leu Phe Ala Arg Met Glu Asp Arg Asn Ser Leu Ser
    290                 295                 300
Asp Glu Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe Glu Gly His
305                 310                 315                 320
Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Phe Tyr Ala Leu Ala Thr
                325                 330                 335
His Pro Glu His Gln Gln Arg Cys Arg Glu Glu Val Gln Ser Ile Leu
            340                 345                 350
Gly Asp Gly Thr Ser Val Thr Trp Asp His Leu Gly Gln Met Pro Tyr
        355                 360                 365
Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Leu Tyr Pro Pro Val Ile
    370                 375                 380
Ser Val Ser Arg Glu Leu Ser Ser Pro Val Thr Phe Pro Asp Gly Arg
385                 390                 395                 400
Ser Ile Pro Lys Gly Ile Thr Ala Thr Ile Ser Ile Tyr Gly Leu His
                405                 410                 415
His Asn Pro Arg Phe Trp Pro Asn Pro Lys Val Phe Asp Pro Ser Arg
            420                 425                 430
Phe Ala Pro Asp Ser Ser His His Ser His Ala Tyr Leu Pro Phe Ser
        435                 440                 445
Gly Gly Ser Arg Asn Cys Ile Gly Lys Gln Phe Ala Met Asn Glu Leu
    450                 455                 460
Lys Val Ala Val Ala Leu Thr Leu Leu Arg Phe Glu Leu Leu Pro Asp
465                 470                 475                 480
Pro Thr Arg Ile Pro Val Pro Ile Ala Arg Leu Val Leu Lys Ser Lys
                485                 490                 495
Asn Gly Ile His Leu Cys Leu Lys Lys Leu Arg
            500                 505
```

<210> 3
<211> 508
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note = synthetic construct

<400> 3

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Met Ser Ala Ser Ala Leu Ser Ser Ile Arg Phe Pro Gly Ser Ile Ser
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Glu Tyr Leu Gln Val Ala Ser Val Leu Ser Leu Leu Leu Leu Leu Phe
            20                  25                  30
Lys Thr Ala Gln Leu Tyr Leu His Arg Gln Trp Leu Leu Ser Ser Thr
        35                  40                  45
Gln Gln Phe Pro Ser Pro Pro Ser His Trp Leu Phe Gly His Lys Ile
    50                  55                  60
Leu Lys Asp Gln Asp Leu Gln Asp Ile Leu Thr Arg Ile Lys Asn Phe
65                  70                  75                  80
Pro Ser Ala Cys Pro Gln Trp Leu Trp Gly Ser Lys Val Arg Ile Gln
                85                  90                  95
Val Tyr Asp Pro Asp Tyr Met Lys Leu Ile Leu Gly Arg Ser Asp Pro
            100                 105                 110
Lys Ala Asn Gly Ser Tyr Arg Phe Leu Ala Pro Trp Ile Gly Arg Gly
        115                 120                 125
Leu Leu Met Leu Asp Gly Gln Thr Trp Phe Gln His Arg Arg Met Leu
    130                 135                 140
Thr Pro Ala Phe His Tyr Asp Ile Leu Lys Pro Tyr Thr Glu Ile Met
145                 150                 155                 160
Ala Asp Ser Val Arg Val Met Leu Asp Lys Trp Glu Gln Ile Val Gly
                165                 170                 175
Gln Asp Ser Thr Leu Glu Ile Phe Arg His Ile Thr Leu Met Thr Leu
            180                 185                 190
Asp Thr Ile Met Lys Cys Ala Phe Ser His Glu Gly Ser Val Gln Leu
        195                 200                 205
Asp Arg Lys Tyr Lys Ser Tyr Ile Gln Ala Val Glu Asp Leu Asn Asp
    210                 215                 220
Leu Val Phe Ser Arg Val Arg Asn Ile Phe His Leu Asn Asp Ile Ile
225                 230                 235                 240
Tyr Arg Val Ser Ser Asn Gly Cys Lys Ala Asn Ser Ala Cys Gln Leu
                245                 250                 255
Ala His Asp His Thr Asp Gln Val Ile Lys Ser Arg Arg Ile Gln Leu
            260                 265                 270
Gln Asp Glu Glu Glu Leu Glu Lys Leu Lys Lys Lys Arg Arg Leu Asp
        275                 280                 285
Phe Leu Asp Ile Leu Leu Phe Ala Arg Met Glu Asn Gly Lys Ser Leu
    290                 295                 300
Ser Asp Lys Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe Glu Gly
305                 310                 315                 320
His Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Phe Tyr Ala Leu Ala
                325                 330                 335
Thr Asn Pro Glu His Gln Gln Arg Cys Arg Lys Glu Ile Gln Ser Leu
            340                 345                 350
Leu Gly Asp Gly Thr Ser Ile Thr Trp Asn Asp Leu Asp Lys Met Pro
        355                 360                 365
Tyr Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Ile Tyr Pro Pro Val
    370                 375                 380
```

```
Pro Ser Val Ser Arg Glu Leu Ser Ser Pro Val Thr Phe Pro Asp Gly
385                 390                 395                 400
Arg Ser Leu Pro Lys Gly Ile His Val Met Leu Ser Phe Tyr Gly Leu
                405                 410                 415
His His Asn Pro Thr Val Trp Pro Asn Pro Glu Val Phe Asp Pro Ser
            420                 425                 430
Arg Phe Ala Pro Gly Ser Ser Arg His Ser His Ser Phe Leu Pro Phe
        435                 440                 445
Ser Gly Gly Ala Arg Asn Cys Ile Gly Lys Gln Phe Ala Met Asn Glu
    450                 455                 460
Leu Lys Val Ala Val Ala Leu Thr Leu Leu Arg Phe Glu Leu Leu Pro
465                 470                 475                 480
Asp Pro Thr Arg Val Pro Ile Pro Ile Pro Arg Ile Val Leu Lys Ser
                485                 490                 495
Lys Asn Gly Ile His Leu His Leu Lys Glu Leu Gln
            500                 505
```

<210> 4
<211> 2116
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
synthetic construct

<400> 4

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caaagaggct gttcaggtcc atcaaccctg gtcttgaaat caagctctgc tcacacccct     180
ctccctcccc caagtaggtg gggcaaccct cctggggttt gcagacagga gggtgttcat     240
tgaaagtgaa ggagagttgg tgatccagaa gctgttgtat catgagtgcc tctgctctga     300
gctccatcag attcccagga agcatctctg agtaccttca agtagcctct gtgctcagcc     360
tgctcctgct gctcttcaag acagcccagc tctacctgca caggcaatgg ctactcagca     420
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ggctctgggg aagcaaagtg cgcattcaag tgtatgaccc tgactacatg aagctgattc     600
tggggagatc agacccaaaa gctaatggtt cctacagatt tctagctccc tggattgggc     660
gtggtttgct tatgctggat ggacagacat ggtttcagca ccgacgaatg ttgaccccag     720
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<210> 5
<211> 519
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
synthetic construct

<400> 5
Met Ser Val Ser Val Leu Ser Pro Ser Arg Leu Leu Gly Asp Val Ser
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Gly Ile Leu Gln Ala Ala Ser Leu Leu Ile Leu Leu Leu Leu Leu Ile
20 25 30
Lys Ala Val Gln Leu Tyr Leu His Arg Gln Trp Leu Leu Lys Ala Leu
35 40 45
Gln Gln Phe Pro Cys Pro Pro Ser His Trp Leu Phe Gly His Ile Gln
50 55 60
Glu Leu Gln Gln Asp Gln Glu Leu Gln Arg Ile Gln Lys Trp Val Glu
65 70 75 80
Thr Phe Pro Ser Ala Cys Pro His Trp Leu Trp Gly Gly Lys Val Arg
85 90 95
Val Gln Leu Tyr Asp Pro Asp Tyr Met Lys Val Ile Leu Gly Arg Ser
100 105 110
Asp Pro Lys Ser His Gly Ser Tyr Arg Phe Leu Ala Pro Trp Ile Gly
115 120 125
Tyr Gly Leu Leu Leu Leu Asn Gly Gln Thr Trp Phe Gln His Arg Arg
130 135 140
Met Leu Thr Pro Ala Phe His Tyr Asp Ile Leu Lys Pro Tyr Val Gly
145 150 155 160
Leu Met Ala Asp Ser Val Arg Val Met Leu Asp Lys Trp Glu Glu Leu
165 170 175
Leu Gly Gln Asp Ser Pro Leu Glu Val Phe Gln His Val Ser Leu Met
180 185 190
Thr Leu Asp Thr Ile Met Lys Cys Ala Phe Ser His Gln Gly Ser Ile
195 200 205
Gln Val Asp Arg Asn Ser Gln Ser Tyr Ile Gln Ala Ile Ser Asp Leu
210 215 220
Asn Asn Leu Val Phe Ser Arg Val Arg Asn Ala Phe His Gln Asn Asp
225 230 235 240
Thr Ile Tyr Ser Leu Thr Ser Ala Gly Arg Trp Thr His Arg Ala Cys
245 250 255
Gln Leu Ala His Gln His Thr Asp Gln Val Ile Gln Leu Arg Lys Ala
260 265 270
Gln Leu Gln Lys Glu Gly Glu Leu Glu Lys Ile Lys Arg Lys Arg His
275 280 285
Leu Asp Phe Leu Asp Ile Leu Leu Leu Ala Lys Met Glu Asn Gly Ser
290 295 300
Ile Leu Ser Asp Lys Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe
305 310 315 320
Glu Gly His Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Leu Tyr Ala
325 330 335

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Leu Ala Thr His Pro Lys His Gln Glu Arg Cys Arg Glu Glu Ile His
            340                 345                 350
Ser Leu Leu Gly Asp Gly Ala Ser Ile Thr Trp Asn His Leu Asp Gln
        355                 360                 365
Met Pro Tyr Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Leu Tyr Pro
    370                 375                 380
Pro Val Pro Gly Ile Gly Arg Glu Leu Ser Thr Pro Val Thr Phe Pro
385                 390                 395                 400
Asp Gly Arg Ser Leu Pro Lys Gly Ile Met Val Leu Leu Ser Ile Tyr
                405                 410                 415
Gly Leu His His Asn Pro Lys Val Trp Pro Asn Pro Glu Val Phe Asp
            420                 425                 430
Pro Phe Arg Phe Ala Pro Gly Ser Ala Gln His Ser His Ala Phe Leu
        435                 440                 445
Pro Phe Ser Gly Gly Ser Arg Asn Cys Ile Gly Lys Gln Phe Ala Met
    450                 455                 460
Asn Glu Leu Lys Val Ala Thr Ala Leu Thr Leu Leu Arg Phe Glu Leu
465                 470                 475                 480
Leu Pro Asp Pro Thr Arg Ile Pro Ile Pro Ile Ala Arg Leu Val Leu
                485                 490                 495
Lys Ser Lys Asn Gly Ile His Leu Arg Leu Arg Arg Leu Pro Asn Pro
            500                 505                 510
Cys Glu Asp Lys Asp Gln Leu
        515
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<210> 6
<211> 2576
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
synthetic construct

<400> 6

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tgctgatcaa ggcagttcag ctctacctgc acaggcagtg gctgctcaaa gccctccagc     180
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<210> 7
<211> 519
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
synthetic construct

<400> 7

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Gly Ile Leu Gln Val Thr Ser Leu Leu Ile Leu Leu Leu Leu Leu Ile
            20                  25                  30
Lys Ala Ala Gln Leu Tyr Leu His Arg Gln Trp Leu Leu Lys Ala Leu
        35                  40                  45
Gln Gln Phe Pro Cys Pro Pro Ser His Trp Leu Phe Gly His Ile Gln
    50                  55                  60
Glu Phe Gln His Asp Gln Glu Leu Gln Arg Ile Gln Glu Arg Val Lys
65                  70                  75                  80
Thr Phe Pro Ser Ala Cys Pro Tyr Trp Ile Trp Gly Gly Lys Val Arg
                85                  90                  95
Val Gln Leu Tyr Asp Pro Asp Tyr Met Lys Val Ile Leu Gly Arg Ser
            100                 105                 110
Asp Pro Lys Ser His Gly Ser Tyr Arg Phe Leu Ala Pro Arg Ile Gly
        115                 120                 125
Tyr Gly Leu Leu Leu Leu Asn Gly Gln Thr Trp Phe Gln His Arg Arg
    130                 135                 140
Met Leu Thr Pro Ala Phe His Asn Asp Ile Leu Lys Pro Tyr Val Gly
145                 150                 155                 160
Leu Met Ala Asp Ser Val Arg Val Met Leu Asp Lys Trp Glu Glu Leu
                165                 170                 175
Leu Gly Gln Asp Ser Pro Leu Glu Val Phe Gln His Val Ser Leu Met
            180                 185                 190
Thr Leu Asp Thr Ile Met Lys Ser Ala Phe Ser His Gln Gly Ser Ile
        195                 200                 205
Gln Val Asp Arg Asn Ser Gln Ser Tyr Ile Gln Ala Ile Ser Asp Leu
```

```
    210                 215                 220
Asn Ser Leu Val Phe Cys Cys Met Arg Asn Ala Phe His Glu Asn Asp
225                 230                 235                 240
Thr Ile Tyr Ser Leu Thr Ser Ala Gly Arg Trp Thr His Arg Ala Cys
                245                 250                 255
Gln Leu Ala His Gln His Thr Asp Gln Val Ile Gln Leu Arg Lys Ala
            260                 265                 270
Gln Leu Gln Lys Glu Gly Glu Leu Glu Lys Ile Lys Arg Lys Arg His
        275                 280                 285
Leu Asp Phe Leu Asp Ile Leu Leu Leu Ala Lys Met Glu Asn Gly Ser
    290                 295                 300
Ile Leu Ser Asp Lys Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe
305                 310                 315                 320
Glu Gly His Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Leu Tyr Ala
                325                 330                 335
Leu Ala Thr His Pro Lys His Gln Glu Arg Cys Arg Glu Glu Ile His
            340                 345                 350
Gly Leu Leu Gly Asp Gly Ala Ser Ile Thr Trp Asn His Leu Asp Gln
        355                 360                 365
Met Pro Tyr Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Leu Tyr Pro
    370                 375                 380
Pro Val Pro Gly Ile Gly Arg Glu Leu Ser Thr Pro Val Thr Phe Pro
385                 390                 395                 400
Asp Gly Arg Ser Leu Pro Lys Gly Ile Met Val Leu Leu Ser Ile Tyr
                405                 410                 415
Gly Leu His His Asn Pro Lys Val Trp Pro Asn Leu Glu Val Phe Asp
            420                 425                 430
Pro Ser Arg Phe Ala Pro Gly Ser Ala Gln His Ser His Ala Phe Leu
        435                 440                 445
Pro Phe Ser Gly Gly Ser Arg Asn Cys Ile Gly Lys Gln Phe Ala Met
    450                 455                 460
Asn Gln Leu Lys Val Ala Arg Ala Leu Thr Leu Leu Arg Phe Glu Leu
465                 470                 475                 480
Leu Pro Asp Pro Thr Arg Ile Pro Ile Pro Ile Ala Arg Leu Val Leu
                485                 490                 495
Lys Ser Lys Asn Gly Ile His Leu Arg Leu Arg Arg Leu Pro Asn Pro
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Cys Glu Asp Lys Asp Gln Leu
        515
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<210> 8
<211> 1872
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
synthetic construct

<400> 8

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<210> 9
<211> 21990
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
synthetic construct

<221> misc_feature
<222> (1)...(21990)
<223> n = g, a, c or t(u)

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